

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 22:28:09 ; Search time 346.26 Seconds
(without alignments)
4455.758 Million cell updates/sec

Title: US-10-073-123-3

Perfect score: 2973

Sequence: 1 ctggctctgctgctccgcg.....tgaaaaaaaaaaaaa 2973

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : Published Applications NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	49.2	1.7	171486	7	US-11-121-086-105
C 6	48.6	1.6	119036	6	US-10-995-561-13314
C 7	48.2	1.6	49979	6	US-10-995-561-13443
C 8	48.2	1.6	105550	6	US-10-750-185-13235
C 9	46.6	1.6	4744	6	US-10-750-185-56531
10	46.6	1.6	26772	6	US-10-995-561-13313
11	46.6	1.6	54946	6	US-10-995-561-13479
12	46.4	1.6	1353	6	US-10-750-185-61820
13	46.4	1.6	184868	7	US-11-121-086-88
C 14	46	1.5	171486	7	US-11-121-086-105
15	45.8	1.5	207908	7	US-11-112-908-21
C 16	45.4	1.5	47572	6	US-10-995-561-13356
17	45	1.5	158692	7	US-11-121-086-30
C 18	44.8	1.5	919	6	US-10-750-185-49202
C 19	44.6	1.5	195998	6	US-10-995-561-13489
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27	43.4	1.5	105550	6	US-10-995-561-13235	Sequence 13235, A
28	43.2	1.5	20317	6	US-10-995-561-13460	Sequence 13460, A
29	43.2	1.5	27902	6	US-10-995-561-13462	Sequence 13462, A
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C 32	42.8	1.4	149419	7	US-11-112-908-49	Sequence 49, Appl
C 33	42.8	1.4	161726	7	US-11-112-908-48	Sequence 48, Appl
C 34	42.8	1.4	161726	7	US-11-112-908-52	Sequence 52, Appl
C 35	42.8	1.4	166111	7	US-11-112-908-47	Sequence 47, Appl
36	42.6	1.4	3206	6	US-10-750-185-34773	Sequence 34773, A
37	42.6	1.4	317876	6	US-10-995-561-13227	Sequence 13227, A
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C 179	37.2	1.3	1317	7	US-11-196-475-167	Sequence 167, App
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C 189	37.2	1.3	184868	7	US-11-121-086-88	Sequence 88, Appl
C 190	37.2	1.3	218821	7	US-11-121-086-31	Sequence 31, Appl
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C 199	37	1.2	1919	6	US-10-415-198A-14	Sequence 14, Appl
C 200	37	1.2	2496	6	US-10-750-185-36044	Sequence 36044, A

ALIGNMENTS

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; Sequence 43043, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 43043
; LENGTH: 1765
; TYPE: DNA
; ORGANISM: Bovine 19866880782548
US-10-750-185-43043

Query Match 5.9%; Score 176; DB 6; Length 1765;
Best Local Similarity 86.6%; Pred. No. 8e-33;
Matches 194; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:39:17 ; Search time 2349.36 Seconds
(without alignments)
10464.498 Million cell updates/sec

Title: US-10-073-123-3
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Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1818	61.2	1818	5	US-10-073-123-1
5	1395.2	46.9	1400	10	US-11-060-756-643
6	1395.2	46.9	1400	10	US-11-060-756-4915
7	448	15.1	996	8	US-10-363-345A-31691
8	448	15.1	996	8	US-10-363-345A-31692
9	448	15.1	996	9	US-10-363-483A-31691
10	448	15.1	996	9	US-10-363-483A-31692
11	430.8	14.5	996	8	US-10-363-483A-31689
12	430.8	14.5	996	8	US-10-363-345A-31690
13	430.8	14.5	996	9	US-10-363-483A-31689
14	430.8	14.5	996	9	US-10-363-483A-31690
15	246.8	8.3	631	7	US-10-152-319A-1304
16	213.2	7.2	416	3	US-09-783-590-7899
17	171	5.8	4901	9	US-10-840-060-132
18	171	5.8	4901	10	US-11-097-143-5456
19	99.2	3.3	8256	10	US-11-097-143-5455
20	90.6	3.0	107	3	US-09-783-590-5787
21	90.4	3.0	357	3	US-09-960-352-14669
22	73.6	2.5	3673778	6	US-10-312-841-2
23	68.2	2.3	8056	8	US-10-473-126-386
Sequence 3, Appli					
Sequence 134, App					
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Sequence 1, Appli					
Sequence 643, App					
Sequence 4915, Ap					
Sequence 31691, A					
Sequence 31692, A					
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Sequence 31689, A					
Sequence 31690, A					
Sequence 31689, A					
Sequence 31690, A					
Sequence 1304, Ap					
Sequence 7899, Ap					
Sequence 132, App					
Sequence 5456, Ap					
Sequence 5455, Ap					
Sequence 5787, Ap					
Sequence 14669, A					
Sequence 2, Appli					
Sequence 386, App					

24	68	2.3	119	7	US-10-430-201-2701	Sequence 2701, Ap
25	68	2.3	119	7	US-10-430-201-2702	Sequence 2702, Ap
c 26	66.6	2.2	8056	8	US-10-473-126-240	Sequence 240, App
27	65.8	2.2	18624	6	US-10-311-455-1675	Sequence 1675, Ap
28	64.4	2.2	5006	3	US-09-837-751-7	Sequence 7, Appli
29	62	2.1	62	8	US-10-758-307-84	Sequence 84, Appl
c 30	61.8	2.1	16217	6	US-10-311-455-597	Sequence 597, App
31	60	2.0	60	3	US-09-908-975-11568	Sequence 11568, A
32	60	2.0	60	3	US-09-908-975-31324	Sequence 31324, A
33	60	2.0	60	3	US-09-908-975-31325	Sequence 31325, A
34	60	2.0	60	3	US-09-908-975-31326	Sequence 31326, A
35	60	2.0	60	3	US-09-908-975-31581	Sequence 31581, A.
36	59.8	2.0	8093	5	US-10-172-086-25	Sequence 25, Appl
37	59.8	2.0	8093	7	US-10-221-714A-157	Sequence 157, App
38	59.8	2.0	8093	7	US-10-240-589C-45	Sequence 45, Appl
39	59.8	2.0	8093	7	US-10-311-507-57	Sequence 57, Appl
40	59.8	2.0	8093	8	US-10-480-846-25	Sequence 25, Appl
41	59.8	2.0	8093	8	US-10-473-126-171	Sequence 171, App
42	59.8	2.0	17213	6	US-10-311-455-1455	Sequence 1455, Ap
c 43	59.4	2.0	8170	6	US-10-240-453-131	Sequence 131, App
44	58.8	2.0	8093	8	US-10-473-126-317	Sequence 317, App
45	58.6	2.0	17967	6	US-10-311-455-988	Sequence 988, App
46	58	2.0	37973	6	US-10-311-455-2170	Sequence 2170, Ap
47	57.6	1.9	15373	6	US-10-311-455-440	Sequence 440, App
c 48	57.2	1.9	6816	8	US-10-723-860-7676	Sequence 7676, Ap
49	57.2	1.9	8056	8	US-10-473-126-240	Sequence 240, App
50	57.2	1.9	17869	6	US-10-311-455-77	Sequence 77, Appl
51	57.2	1.9	17869	7	US-10-257-166-1	Sequence 1, Appli
52	56.6	1.9	8170	6	US-10-240-453-132	Sequence 132, App
53	56.4	1.9	960	5	US-10-198-846-6381	Sequence 6381, Ap
54	55.6	1.9	562	4	US-09-925-065A-138840	Sequence 138840,
c 55	55.4	1.9	5875	6	US-10-311-455-262	Sequence 262, App
56	55.4	1.9	8056	8	US-10-473-126-386	Sequence 386, App
57	55.2	1.9	6121	6	US-10-240-485-31	Sequence 31, Appl
58	55.2	1.9	6121	7	US-10-221-613-45	Sequence 45, Appl
59	55	1.8	9155	6	US-10-311-455-435	Sequence 435, App
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64	54.2	1.8	16602	6	US-10-311-455-699	Sequence 699, App
65	54.2	1.8	18357	7	US-10-433-793-113	Sequence 113, App
66	54	1.8	3287	8	US-10-473-126-332	Sequence 332, App
c 67	53.4	1.8	586	4	US-09-925-065A-188822	Sequence 188822,
c 68	53.4	1.8	1342	4	US-09-925-065A-703795	Sequence 703795,
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70	53.4	1.8	385320	8	US-10-741-600-17796	Sequence 17796, A
c 71	53	1.8	586	4	US-09-925-065A-188819	Sequence 188819,
c 72	53	1.8	586	4	US-09-925-065A-188820	Sequence 188820,
c 73	53	1.8	586	4	US-09-925-065A-188821	Sequence 188821,
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75	52.8	1.8	6106	6	US-10-311-455-1445	Sequence 1445, Ap
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77	52.8	1.8	6106	7	US-10-221-714A-151	Sequence 151, App
78	52.8	1.8	9502	7	US-10-221-714A-456	Sequence 456, App
79	52.8	1.8	11790	6	US-10-311-455-515	Sequence 515, App
80	52.8	1.8	14307	6	US-10-311-455-701	Sequence 701, App
81	52.6	1.8	5696	6	US-10-311-455-811	Sequence 811, App
82	52.6	1.8	9524	6	US-10-257-166-75	Sequence 75, Appl
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84	52.4	1.8	1882	7	US-10-767-701-12741	Sequence 12741, A
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88	52.2	1.8	8964	7	US-10-221-613-238	Sequence 238, App
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c 90	52.2	1.8	513509	3	US-09-754-853A-4	Sequence 4, Appli
91	52	1.7	6167	6	US-10-240-453-244	Sequence 1, Appli
92	52	1.7	3673778	6	US-10-312-841-1	Sequence 1620, Ap
93	51.8	1.7	6024	6	US-10-311-455-1620	Sequence 259, App
94	51.8	1.7	7047	6	US-10-240-453-259	Sequence 860, App
95	51.8	1.7	16439	6	US-10-311-455-860	Sequence 1307, Ap
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97	51.6	1.7	6866	6	US-10-311-455-640	Sequence 640, App
98	51.6	1.7	7346	6	US-10-311-455-318	Sequence 318, App
99	51.6	1.7	7667	7	US-10-221-714A-55	Sequence 55, Appl
100	51.6	1.7	19659	6	US-10-311-455-740	Sequence 740, App
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c 103	51.4	1.7	3252	5	US-10-027-632-113788	Sequence 113788,
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107	51.4	1.7	11422	6	US-10-311-455-191	Sequence 191, App
108	51.4	1.7	11422	7	US-10-257-166-17	Sequence 17, Appl
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110	51.2	1.7	5001	5	US-10-172-086-69	Sequence 69, Appl
111	51.2	1.7	5001	6	US-10-240-452-73	Sequence 73, Appl
112	51.2	1.7	5001	7	US-10-311-507-33	Sequence 33, Appl
113	51.2	1.7	5001	8	US-10-480-846-69	Sequence 69, Appl
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115	51.2	1.7	34688	7	US-10-433-793-90	Sequence 90, Appl
116	51.2	1.7	61944	6	US-10-329-079-34	Sequence 34, Appl
c 117	51	1.7	387	8	US-10-425-115-97640	Sequence 97640, A
c 118	51	1.7	4661	7	US-10-433-793-52	Sequence 52, Appl
119	51	1.7	5360	6	US-10-311-455-1909	Sequence 1909, Ap
120	51	1.7	5360	7	US-10-240-589C-105	Sequence 105, App
121	51	1.7	5928	6	US-10-311-455-2059	Sequence 2059, Ap
122	51	1.7	6182	6	US-10-311-455-1988	Sequence 1988, Ap
123	51	1.7	14307	6	US-10-311-455-702	Sequence 702, App
124	51	1.7	34688	7	US-10-433-793-89	Sequence 89, Appl
c 125	51	1.7	3673778	6	US-10-312-841-2	Sequence 2, Appli
c 126	50.8	1.7	2181	8	US-10-706-635-40	Sequence 40, Appl
127	50.8	1.7	3287	8	US-10-473-126-186	Sequence 186, App
128	50.8	1.7	5430	7	US-10-221-714A-14	Sequence 14, Appl
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130	50.8	1.7	32329	7	US-10-374-903A-1	Sequence 1, Appli
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132	50.6	1.7	7306	6	US-10-311-455-1609	Sequence 1609, Ap
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134	50.6	1.7	9539	6	US-10-240-453-53	Sequence 53, Appl
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c 142	50.2	1.7	8979	6	US-10-311-455-757	Sequence 757, App
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c 144	50.2	1.7	13377	6	US-10-311-455-1436	Sequence 1436, Ap
c 145	50.2	1.7	13377	7	US-10-221-714A-198	Sequence 198, App
146	49.8	1.7	1501	8	US-10-473-126-328	Sequence 328, App
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148	49.8	1.7	7441	7	US-10-257-166-140	Sequence 140, App
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153	49.8	1.7	14861	6	US-10-311-455-1167	Sequence 1167, Ap
154	49.8	1.7	14861	7	US-10-221-613-161	Sequence 161, App
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157	49.6	1.7	6030	5	US-10-239-676-163	Sequence 163, App
158	49.6	1.7	6030	6	US-10-240-453-185	Sequence 185, App
159	49.6	1.7	6030	7	US-10-221-613-309	Sequence 309, App
160	49.6	1.7	6076	7	US-10-221-714A-386	Sequence 386, App
161	49.6	1.7	7442	7	US-10-221-714A-409	Sequence 409, App
162	49.6	1.7	9728	6	US-10-311-455-1876	Sequence 1876, Ap
163	49.6	1.7	9728	7	US-10-257-166-174	Sequence 174, App
164	49.6	1.7	11334	6	US-10-311-455-1205	Sequence 1205, Ap
c 165	49.6	1.7	16811	6	US-10-311-455-1920	Sequence 1920, Ap
166	49.6	1.7	17131	6	US-10-311-455-1026	Sequence 1026, Ap
167	49.6	1.7	40862	6	US-10-311-455-2046	Sequence 2046, Ap
168	49.6	1.7	83391	7	US-10-433-793-123	Sequence 123, App
169	49.6	1.7	335199	9	US-10-496-011-4	Sequence 4, Appli
170	49.4	1.7	7849	7	US-10-240-589C-88	Sequence 88, Appl
171	49.4	1.7	19082	6	US-10-311-455-600	Sequence 600, App
172	49.4	1.7	37515	7	US-10-433-793-28	Sequence 28, Appl
173	49.2	1.7	5488	6	US-10-311-455-1429	Sequence 1429, Ap
174	49.2	1.7	13038	6	US-10-311-455-1247	Sequence 1247, Ap
175	49.2	1.7	13427	6	US-10-311-455-1899	Sequence 1899, Ap
176	49	1.6	870	5	US-10-027-632-32490	Sequence 32490, A
177	49	1.6	870	6	US-10-027-632-32490	Sequence 32490, A
c 178	49	1.6	956	4	US-09-925-065A-717311	Sequence 717311,
c 179	49	1.6	956	4	US-09-925-065A-717312	Sequence 717312,
c 180	49	1.6	1026	4	US-09-925-065A-80193	Sequence 80193, A
c 181	49	1.6	6131	6	US-10-311-455-863	Sequence 863, App
182	49	1.6	6203	5	US-10-239-676-183	Sequence 183, App
183	49	1.6	6203	6	US-10-240-453-273	Sequence 273, App
c 184	49	1.6	12405	5	US-10-239-676-35	Sequence 35, Appl
c 185	49	1.6	12405	6	US-10-240-453-43	Sequence 43, Appl
c 186	49	1.6	12405	7	US-10-221-613-101	Sequence 101, App
c 187	49	1.6	49979	7	US-10-741-601-5746	Sequence 5746, Ap
c 188	49	1.6	49979	8	US-10-741-600-17905	Sequence 17905, A
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c 190	48.8	1.6	875	9	US-10-779-543-8007	Sequence 8007, Ap
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193	48.8	1.6	6208	6	US-10-311-455-167	Sequence 167, App
c 194	48.8	1.6	6676	7	US-10-433-793-44	Sequence 44, Appl
195	48.8	1.6	13814	6	US-10-311-455-1166	Sequence 1166, Ap
196	48.8	1.6	27890	7	US-10-741-601-5686	Sequence 5686, Ap
197	48.8	1.6	27890	8	US-10-741-600-17751	Sequence 17751, A
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; Publication No. US20030032027A1						
; GENERAL INFORMATION:						
; APPLICANT: LI, Jing						
; APPLICANT: POWERS, Scott						
; TITLE OF INVENTION: AMPLIFIED CANCER GENE WIP1						
; FILE REFERENCE: 38002-0023						
; CURRENT APPLICATION NUMBER: US/10/073.123						
; CURRENT FILING DATE: 2002-02-12						
; PRIOR APPLICATION NUMBER: US 60/268,362						
; PRIOR FILING DATE: 2001-02-14						
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QY	121	GTTCGCGCGGAGCGCCTAGTGTGTCTCCGCCCGCGGATTCGCGGGTTCGCTGGGACC	180			
Db	121	GTTCGCGCGGAGCGCCTAGTGTGTCTCCGCCCGCGGATTCGCGGGTTCGCTGGGACC	180			

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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	57.4	1.9	601	3	US-09-949-016-37150
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8	57.4	1.9	601	3	US-09-949-016-146136
9	57.4	1.9	601	3	US-09-949-016-146404
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11	57.4	1.9	205044	3	US-09-949-016-15852
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ALIGNMENTS

RESULT 1

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; Sequence 2226, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2226
; LENGTH: 2961
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2226

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2957; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Post-processing: Minimum Match 0%
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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147	345.6	11.6	753	10	AG520850	Mus muscu	
148	345.2	11.6	729	1	AJ657690	AJ657690	
C 149	341.2	11.5	515	2	BE109971	UI-R-BJ1-	
150	340.4	11.4	500	3	BI991619	4103-24.M	
C 151	339	11.4	484	2	BG181388	RST228.At	
152	338.8	11.4	440	2	BB847793	BB847793	
153	337.8	11.4	748	7	CK237744	AGENCOURT	
154	336.8	11.3	868	6	CB845030	M2PN-0596	
155	336.2	11.3	435	1	AA608209	vm89b06.r	
156	336.2	11.3	648	1	AL879406	AL879406	
C 157	330	11.1	354	1	AI678492	tu83a11.x	
C 158	329.8	11.1	378	3	BM150404	TCBAP1D08	
159	327.8	11.0	522	5	BX527529	BX527529	
160	325.8	11.0	903	5	BU110146	603127635	
161	322.8	10.9	426	1	AA097213	mk09h04.r	
162	322.6	10.9	432	2	BP556390	UI-R-AJ-e	
163	320.4	10.8	447	2	BE927292	RC1-CT028	
C 164	320.2	10.8	887	5	BU217243	603105944	
165	319.2	10.7	833	5	BU746851	CH3#007.D	
166	318.4	10.7	368	1	AA396939	mr41dl1.r	
C 167	317	10.7	334	1	AA722551	zg80h07.s	
168	316.8	10.7	521	1	AA124664	mp79e07.r	

169	316.6	10.6	716	8	DT110018	JGI_ANNO6
170	314.8	10.6	357	2	BF995912	RCS-GN019
171	314.6	10.6	488	2	BG101153	uy20a08.y
C 172	312.8	10.5	316	1	AA399213	zt57b04.s
173	312	10.5	353	2	BF515693	UI-H-BW1-
174	312	10.5	765	5	BU115028	603130876
175	311.8	10.5	431	4	AK187243	Mus muscu
176	310.6	10.4	610	6	CD535550	LeukON5_6
177	306	10.3	385	5	BY295911	BY295911
178	305	10.3	732	5	BU375100	603812175
179	298.4	10.0	396	1	AI020281	ub16b02.r
180	296	10.0	619	7	CO786028	BL285A_H1
181	293	9.9	357	4	AK181083	Mus muscu
182	291.8	9.8	745	5	BU457443	603772584
183	291	9.8	745	5	BU312040	603544376
184	290	9.8	466	1	AA985793	ua66g10.r
185	288.4	9.7	829	5	BU211059	603102418
186	284.6	9.6	363	1	AJ694597	AJ694597
187	284.4	9.6	634	1	AL729451	AL729451
188	284.2	9.6	664	1	AL729975	AL729975
C 189	283.2	9.5	658	1	AL729396	AL729396
190	281.6	9.5	914	5	BU911792	AGENCOURT
191	281	9.5	284	1	AA310681	EST181495
192	277.8	9.3	452	1	AA116254	mq06e11.r
193	276	9.3	890	5	BU907104	AGENCOURT
C 194	271	9.1	738	2	BG076151	H3156C03-
C 195	268.8	9.0	540	7	CK977151	CK977151
196	267.2	9.0	769	7	CV483699	AGENCOURT
C 197	265.2	8.9	421	7	CK346041	L0800B09-
198	265.2	8.9	442	6	CB427346	602917.MA
199	265.2	8.9	921	5	BU906849	AGENCOURT
C 200	264.2	8.9	694	3	BQ193242	UI-R-DR1-

ALIGNMENTS

RESULT 1	CR618625	2927 bp	linear	HTC 21-JUL-2004
LOCUS	CR618625 full-length cDNA clone CS0DF030YI21 of Fetal brain of Homo sapiens (human) .			
DEFINITION	CR618625			
ACCESSION	CR618625.1 GI:50499432			
VERSION	HTC; CNSLT_cDNA.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 2927)			
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue			
REFERENCE	2 (bases 1 to 2927)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES	Location/Qualifiers			
source	1. .2927 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"			

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:22:00 ; Search time 1735.03 Seconds
(without alignments)
11420.080 Million cell updates/sec

Title: US-10-073-123-3
Perfect score: 2973
Sequence: 1 ctggctctgctgcgtccggc.....tgaaaaaaaaaaaaaaa 2973

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2973	100.0	2973	6	ABS52510 Human amp
2	2973	100.0	2973	10	ADK11345 Human Wip
3	2946	99.1	2961	10	ADK41027 Novel hum
4	2946	99.1	2961	13	ADR15741 Kinase 60
5	1472	49.5	1719	4	AAK91530 Human dig
6	448	15.1	996	6	ABQ45100 Oligonuc1
7	448	15.1	996	6	ABQ45101 Oligonuc1
8	430.8	14.5	996	6	ABQ45098 Oligonuc1
9	430.8	14.5	996	6	ABQ45099 Oligonuc1
10	370.8	12.5	478	10	ADD35192 Mouse mit
11	319	10.7	366	13	ADU09876 Solid tum
12	292	9.8	292	10	ADK11965 Breast ca
13	292	9.8	292	14	ACL61577 Human col
14	268	9.0	735	10	ADD35191 Mouse mit
15	246.8	8.3	631	10	ABT41602 Toxicity
16	171	5.8	4901	4	ABL05477 Drosophil
17	171	5.8	4901	10	ADK11343 Drosophil
18	99.2	3.3	8256	4	ABL05476 Drosophil
19	90.4	3.0	357	8	ABX49504 Bovine ES

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 13:46:36 ; Search time 14916.5 Seconds
(without alignments)
11329.436 Million cell updates/sec

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Perfect score: 2973
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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11: gb_ey:*
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13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2887	97.1	2902	8	BC016480
6	2850.6	95.9	2865	8	BC033893
7	2775.8	93.4	3070	8	BC042418
8	1989.6	66.9	2169	8	AB168475
9	1837	61.8	2908	6	BC051966
10	1818	61.2	1818	6	AX662143 Sequence
11	1816	61.1	1818	8	BT009780
12	1816	61.1	1818	11	AY888848
13	1816	61.1	1818	11	AY888849
14	1496	50.3	160854	8	AC110602
15	1496	50.3	174711	14	AC025515
16	1496	50.3	185101	14	AC079202
17	1490.4	50.1	2023	9	BC023492
18	1410.4	47.4	1968	9	AF200464 Mus muscu

92	63	2.1	349980	6	AX3444567	AX3444567 Sequence	165	58.8	2.0	42478	14	AC157757	AC157757 Medicago
c 93	62.8	2.1	183445	14	AC026212	AC026212 Homo sapi	c 166	58.8	2.0	110000	1	BA000021_3	Continuation (4 of
94	62.8	2.1	185500	14	CR854827	CR854827 Danio rer	c 167	58.8	2.0	125467	15	AC135800	AC135800 Medicago
95	62.8	2.1	250053	2	AE014825	AE014825 Plasmodiu	168	58.8	2.0	125567	15	AC146940	AC146940 Medicago
96	62.4	2.1	217621	14	BX901924	BX901924 Danio rer	c 169	58.8	2.0	129585	15	AC138017	AC138017 Medicago
c 97	62.4	2.1	221958	14	CR847903	CR847903 Danio rer	170	58.6	2.0	17967	6	AX345917	AX345917 Sequence
c 98	62.2	2.1	76568	2	MBREV	AF538053 Monosiga	171	58.6	2.0	85779	15	SCE011856	AJ011856 Saccharom
99	62	2.1	62	6	CQ876234	CQ876234 Sequence	172	58.6	2.0	88549	2	AC116924	AC116924 Dictyoste
c 100	62	2.1	94784	8	AL355309	AL355309 Human DNA	173	58.4	2.0	67970	2	PFMAL1P3	AL031746 Plasmodiu
c 101	61.8	2.1	16217	6	AX345526	AX345526 Sequence	174	58.4	2.0	105238	8	AC011458	AC011458 Homo sapi
c 102	61.8	2.1	343050	2	PFA929353	AL929353 Plasmodiu	c 175	58.4	2.0	106763	8	AP002091	AP002091 Homo sapi
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c 105	61	2.1	85779	15	SCE011856	AJ011856 Saccharom	c 178	58.4	2.0	117101	8	AC004061	AC004061 Homo sapi
c 106	61	2.1	155048	14	CR450727	CR450727 Danio rer	c 179	58.4	2.0	141721	14	AC149953	AC149953 Strongylo
c 107	60.8	2.0	66933	14	AC138074	AC138074 Homo sapi	c 180	58.4	2.0	176184	14	CR352229	CR352229 Danio rer
108	60.8	2.0	156721	8	AC026839	AC026839 Homo sapi	c 181	58.4	2.0	177301	8	AC103949	AC103949 Homo sapi
c 109	60.4	2.0	197142	14	CR388410	CR388410 Danio rer	c 182	58.4	2.0	191041	8	AC091742	AC091742 Homo sapi
c 110	60.2	2.0	1192	8	HS323759	AJ323759 Homo sapi	183	58.4	2.0	191121	14	AC083952	AC083952 Homo sapi
c 111	60.2	2.0	164399	2	PFMAL3P6	Z98551 Plasmodiu	184	58.4	2.0	210821	14	CR847947	CR847947 Danio rer
112	60	2.0	60	6	CQ541933	CQ541933 Sequence	185	58.4	2.0	250078	2	AE014829	AE014829 Plasmodiu
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c 117	60	2.0	44352	2	AF098501	AF098501 Caenorhab	c 190	58	2.0	15470	2	AC117073	AC117073 Dictyoste
c 118	60	2.0	154614	14	CR855263	CR855263 Danio rer	191	58	2.0	37973	6	AX347099	AX347099 Sequence
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124	59.8	2.0	8093	6	AX251189	AX251189 Sequence	197	57.8	1.9	576	10	BV358102	BV358102 S231P6185
125	59.8	2.0	8093	6	AX281166	AX281166 Sequence	c 198	57.8	1.9	296483	14	AC069258	AC069258 Homo sapi
126	59.8	2.0	8093	6	AX347410	AX347410 Sequence	c 199	57.6	1.9	2000	6	AX655393	AX655393 Sequence
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c 137	59.8	2.0	146570	2	AC117076	AC117076 Dictyoste							
c 138	59.8	2.0	253924	2	AE014822	AE014822 Plasmodiu							
c 139	59.8	2.0	341050	2	PFA929357	AL929357 Plasmodiu							
140	59.6	2.0	10049	1	AF291051	AF291051 Carsonell							
c 141	59.6	2.0	250078	2	AE014829	AE014829 Plasmodiu							
142	59.6	2.0	251448	2	AE014819	AE014819 Plasmodiu							
143	59.6	2.0	256879	2	AC116982	AC116982 Dictyoste							
c 144	59.4	2.0	8170	6	AX323643	AX323643 Sequence							
c 145	59.4	2.0	106763	8	AP002091	AP002091 Homo sapi							
146	59.4	2.0	144759	8	HS352A20	AL021939 Human DNA							
c 147	59.4	2.0	157630	8	AC135012	AC135012 Homo sapi							
c 148	59.4	2.0	181792	8	AC098822	AC098822 Homo sapi							
149	59.4	2.0	205309	14	CR847836	CR847836 Danio rer							
c 150	59.2	2.0	30157	8	AC073242	AC073242 Homo sapi							
c 151	59.2	2.0	122890	15	AP005672	AP005672 Physcomit							
152	59.2	2.0	174359	14	CR855123	CR855123 Danio rer							
c 153	59.2	2.0	178207	8	AC140172	AC140172 Homo sapi							
c 154	59.2	2.0	232822	14	AC120204	AC120204 Pan trogl							
155	59	2.0	1141	6	AR579680	AR579680 Sequence							
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RESULT 1	AX662145	AX662145	Sequence 3 from Patent WO02064838.	2973 bp	DNA	linear	PAT 22-MAR-2003
LOCUS	AX662145	Sequence 3 from Patent WO02064838.					
DEFINITION	AX662145	Sequence 3 from Patent WO02064838.					
ACCESSION	AX662145	Sequence 3 from Patent WO02064838.					
VERSION	AX662145.1	GI:29163066					
KEYWORDS	AX662145.1	GI:29163066					
SOURCE	AX662145	Sequence 3 from Patent WO02064838.					
ORGANISM	AX662145	Sequence 3 from Patent WO02064838.					
REFERENCE	AX662145	Sequence 3 from Patent WO02064838.					
AUTHORS	AX662145	Sequence 3 from Patent WO02064838.					
TITLE	AX662145	Sequence 3 from Patent WO02064838.					
JOURNAL	AX662145	Sequence 3 from Patent WO02064838.					
FEATURES	AX662145	Sequence 3 from Patent WO02064838.					
source	AX662145	Sequence 3 from Patent WO02064838.					
ORIGIN	AX662145	Sequence 3 from Patent WO02064838.					

Query Match	100.0%;	Score 2973;	DB 6;	Length 2973;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2973;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	CTGGCTCTGCTCGCTCCGGCGGCTCCGGCCAGCTCTCGCGGACAAAGTCCAGACATCGCGC	60
Db	1	CTGGCTCTGCTCGCTCCGGCGGCTCCGGCCAGCTCTCGCGGACAAAGTCCAGACATCGCGC	60

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 22:28:09 ; Search time 211.74 Seconds
(without alignments)
4455.758 Million cell updates/sec

Title: US-10-073-123-1
Perfect score: 1818
Sequence: 1 atggcggggctgtactcgt.....aaactgttctgtgttctga 1818

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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C 2	45.4	2.5 47572 6	US-10-995-561-13356 Sequence 13356, A
C 3	44.6	2.5 195998 6	US-10-995-561-13489 Sequence 13489, A
C 4	42.4	2.3 172543 7	US-11-121-086-6 Sequence 6, Appli
C 5	42	2.3 191684 7	US-11-121-086-2 Sequence 2, Appli
C 6	41	2.3 153376 7	US-11-121-086-5 Sequence 5, Appli
C 7	41	2.3 172543 7	US-11-121-086-6 Sequence 6, Appli
C 8	40.2	2.2 936 6	US-10-750-185-43199 Sequence 43199, A
C 9	39.8	2.2 180654 7	US-11-121-086-58 Sequence 58, Appl
C 10	39.4	2.2 5801 7	US-11-000-463-580 Sequence 580, App
C 11	39.2	2.2 12277 6	US-10-477-507A-3 Sequence 3, Appli
C 12	38.8	2.1 11070 7	US-11-075-185-34 Sequence 34, Appl
C 13	38.8	2.1 78869 7	US-11-075-185-1 Sequence 1, Appli
C 14	38.4	2.1 2457 6	US-10-955-554A-102 Sequence 102, App
C 15	38.2	2.1 2584 6	US-10-821-234-836 Sequence 836, App
C 16	37.8	2.1 3851 7	US-11-090-739-119 Sequence 119, App
C 17	37.4	2.1 170995 7	US-11-121-086-35 Sequence 35, Appl
C 18	37.2	2.0 1356 6	US-10-750-185-32858 Sequence 32858, A
C 19	37	2.0 1063 6	US-10-750-185-48014 Sequence 48014, A
C 20	37	2.0 3671 6	US-10-131-826A-141 Sequence 141, App
C 21	36.8	2.0 1377 6	US-10-618-320A-2 Sequence 2, Appli
C 22	36.8	2.0 1413 6	US-10-979-821-13 Sequence 13, Appl
C 23	36.6	2.0 2262 6	US-10-821-234-726 Sequence 726, App

24	36.6	2.0	2276	6	US-10-131-826A-9	Sequence 9, Appli
25	36.6	2.0	2492	6	US-10-821-234-629	Sequence 629, App
26	36.6	2.0	4608	6	US-10-821-234-137	Sequence 137, App
C 27	36.4	2.0	10968	7	US-11-075-185-35	Sequence 35, Appl
28	36.4	2.0	13672	7	US-11-055-035-2	Sequence 2, Appli
29	36.4	2.0	101001	6	US-10-995-561-13255	Sequence 13255, A
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C 31	36.2	2.0	1280	6	US-10-802-796-4	Sequence 4, Appli
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36	36	2.0	12591	6	US-10-995-561-13415	Sequence 13415, A
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C 41	36	2.0	415117	6	US-10-995-561-13274	Sequence 13274, A
C 42	35.8	2.0	165857	7	US-11-121-086-34	Sequence 34, Appl
C 43	35.8	2.0	171936	6	US-10-933-025-24	Sequence 24, Appl
44	35.6	2.0	1110	6	US-10-432-483-14	Sequence 14, Appl
C 45	35.6	2.0	1830	7	US-11-064-774A-120	Sequence 120, App
46	35.6	2.0	8651	6	US-10-432-483-48	Sequence 48, Appl
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53	35.4	1.9	11462	7	US-11-140-417-22	Sequence 22, Appl
54	35.4	1.9	61718	6	US-10-995-561-13326	Sequence 13326, A
C 55	35.2	1.9	957	7	US-11-060-029-20	Sequence 20, Appl
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C 57	35.2	1.9	1306	7	US-11-060-029-14	Sequence 14, Appl
58	35.2	1.9	172147	7	US-11-112-908-22	Sequence 22, Appl
59	35.2	1.9	188682	7	US-11-112-908-23	Sequence 23, Appl
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C 65	35	1.9	161726	7	US-11-112-908-52	Sequence 52, Appl
C 66	35	1.9	165857	7	US-11-121-086-34	Sequence 34, Appl
C 67	35	1.9	170189	7	US-11-112-908-50	Sequence 50, Appl
C 68	34.8	1.9	1191	6	US-10-750-185-51530	Sequence 51530, A
69	34.8	1.9	1782	6	US-10-750-185-57415	Sequence 57415, A
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C 80	34.6	1.9	9066	7	US-11-129-143-48	Sequence 48, Appl
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C 95	34.4	1.9	268685	6	US-10-933-025-22	Sequence 22, Appl
C 96	34.2	1.9	1490	6	US-10-533-355-7	Sequence 7, Appli

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 200 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1818	100.0	2973	9	US-10-840-060-134
5	464	25.5	1400	10	US-11-060-756-643
6	464	25.5	1400	10	US-11-060-756-4915
7	316.8	17.4	996	8	US-10-363-345A-31689
8	316.8	17.4	996	8	US-10-363-345A-31690
9	316.8	17.4	996	9	US-10-363-483A-31689
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14	301	16.6	996	9	US-10-363-483A-31692
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40	47.2	2.6	164051	9	US-10-760-493-18	Sequence 18, Appl
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53	45.8	2.5	462	7	US-10-437-963-77570	Sequence 77570, A
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55	45.8	2.5	1755	6	US-10-369-493-40542	Sequence 40542, A
56	45.6	2.5	352	8	US-10-425-115-70912	Sequence 70912, A
57	45.6	2.5	1167	7	US-10-437-963-63792	Sequence 63792, A
58	45.6	2.5	3459	7	US-10-311-795-3	Sequence 3, Appli
59	45.6	2.5	3459	9	US-10-756-149-1720	Sequence 1720, Ap
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61	45.4	2.5	468	7	US-10-282-122A-25614	Sequence 25614, A
62	45.4	2.5	540	7	US-10-437-963-32260	Sequence 32260, A
63	45.4	2.5	777	6	US-10-029-386-20524	Sequence 20524, A
64	45.4	2.5	5208	9	US-10-937-379-42	Sequence 42, Appl
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91	44	2.4	2079	3	US-09-037-657-43	Sequence 43, Appl
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93	43.8	2.4	1632	7	US-10-437-963-52545	Sequence 52545, A
94	43.8	2.4	1866	7	US-10-437-963-36012	Sequence 36012, A
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OM nucleic - nucleic search, using sw model

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10335.313 Million cell updates/sec

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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	46.4	2.6	688	3	US-09-621-011-73 Sequence 73, Appl
7	45.8	2.5	700	3	US-09-236-097-7 Sequence 7, Appli
8	45.8	2.5	43117	3	US-09-949-016-17589 Sequence 17589, A
9	45.4	2.5	7218	2	US-08-232-463-14 Sequence 14, Appl
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c 173	39.2	2.2	1018	2	US-08-443-952-7	Sequence 7, Appli
c 174	39.2	2.2	1018	2	US-08-443-130-7	Sequence 7, Appli
c 175	39.2	2.2	1018	3	US-08-898-911-7	Sequence 7, Appli
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c 181	39.2	2.2	4180	3	US-09-814-915A-93	Sequence 93, Appl
c 182	39.2	2.2	4180	3	US-09-949-002-103	Sequence 103, App
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c 186	39.2	2.2	15044	3	US-09-949-002-710	Sequence 710, App
c 187	39.2	2.2	136917	3	US-09-949-016-16369	Sequence 16369, A
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190	39	2.1	5312	3	US-09-902-540-4775	Sequence 4775, Ap
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193	39	2.1	93532	3	US-09-949-016-15944	Sequence 15944, A
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ALIGNMENTS

RESULT 1

US-09-949-016-2226
; Sequence 2226, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2226
; LENGTH: 2961
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2226

Query Match 100.0%; Score 1818; DB 3; Length 2961;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1818; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	ATGAGGACGTTACTCAAAATCGTTGTGGAGCCCGAACCGAGCTGAAGAAAAGCCCTCG	120
Db	265	ATGAGGACGTTACTCAAAATCGTTGTGGAGCCCGAACCGAGCTGAAGAAAAGCCCTCG	324
Qy	121	CCGCGGGCGTGTCTCAGCCGTTGCTCCGCGCGCTCCGCGCGCTCCGCGCGCTCCGCGCG	180

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Title: US-10-073-123-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1212.4	66.7	1593	11	DQ029467 Pan trogl
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157	236.6	13.0	466	1	AA985793	ua66g10.r	
158	236.2	13.0	801	6	CB310370	AGENCOURT	
159	234.8	12.9	682	5	BW262305	BW262305	
C 160	233.8	12.9	421	7	CK346041	L0800B09-	
161	233.2	12.8	896	7	CK799175	AGENCOURT	
162	231.4	12.7	887	7	CK797067	AGENCOURT	
163	227.8	12.5	452	1	AA116254	mq06e11.r	
164	227.8	12.5	521	1	AA124664	mp79e07.r	
165	225.4	12.4	836	1	AM031095	AM031095	
C 166	224.8	12.4	635	2	BB616277	BB616277	
167	224	12.3	739	7	CJ354166	CJ354166	
168	219.8	12.1	457	1	AU280469	AU280469	

169	219.8	12.1	864	7	CJ375970	CJ375970	
170	217.2	11.9	442	6	CB427346	602917.MA	
171	216.2	11.9	528	6	CB273832	mai85c04.	
172	216.2	11.9	846	7	CK796994	AGENCOURT	
173	214	11.8	597	3	BI462848	603207827	
174	212.8	11.7	747	7	CK694781	ZF101-P00	
175	210.6	11.6	511	1	AW639011	bl177e05.w	
176	209	11.5	890	6	CA790116	AGENCOURT	
C 177	208.8	11.5	813	9	CC570133	CH240.445	
178	208	11.4	800	9	BZ274588	CH230-355	
179	204.6	11.3	915	6	CD778547	EST649908	
180	203.8	11.2	619	6	CA378435	657313.NC	
181	203.4	11.2	455	7	CK614315	LPse.G15	
182	201.6	11.1	444	5	BY382594	BY382594	
183	201.6	11.1	838	7	CR564245	CR564245	
184	200.8	11.0	873	7	CN327806	AGENCOURT	
185	199.2	11.0	761	2	BI079680	602874630	
186	199	10.9	666	5	BW732636	BW732636	
187	198.6	10.9	644	3	BM426588	pgf2n.pk0	
188	197.6	10.9	447	2	BE927292	RC1-CT028	
189	197	10.8	825	6	CF253530	mdvn104.h	
190	195.8	10.8	376	2	BG100789	uy14h01.y	
191	195.2	10.7	563	8	DN508138	HL0200070	
192	195	10.7	397	1	AA412202	zt57a08.f	
193	193.6	10.6	680	5	BU318102	603486881	
194	193	10.6	294	1	BB045763	BB045763	
195	190.4	10.5	355	2	BF715165	BF715165	
196	189.2	10.4	811	7	CN843661	mab05h12.	
197	187	10.3	415	2	BB680262	BB680262	
198	185.6	10.2	714	5	BW259302	BW259302	
199	185.4	10.2	827	6	CD750838	AGENCOURT	
200	183.6	10.1	746	5	BW272782	BW272782	

ALIGNMENTS

RESULT 1	DQ029466	1818 bp	DNA	linear	GSS 02-JUN-2005
LOCUS	DQ029466	Homo sapiens PPM1D gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	DQ029466	genomic survey sequence.			
ACCESSION	DQ029466				
VERSION	DQ029466.1	GI:66880670			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1818)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees				
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 1818)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
FEATURES	Location/Qualifiers				
source	1..1818				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 15:22:00 ; Search time 1060.97 Seconds
(without alignments)
11420.080 Million cell updates/sec

Title: US-10-073-123-1
Perfect score: 1818
Sequence: 1 atggcggggtgtactcgt.....aaactgttgtgttgctga 1818

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1818	100.0	2961	10 ADK41027	Adk41027 Novel hum
2	1818	100.0	2961	13 ADR15741	Adr15741 Kinase 60
3	1818	100.0	2973	6 ABS52510	Abs52510 Human amp
4	1818	100.0	2973	10 ADK11345	Adk11345 Human wip
5	536	29.5	1719	4 AAK91530	Aak91530 Human dig
6	370.8	20.4	478	10 ADD35192	Add35192 Mouse mit
7	316.8	17.4	996	6 ABQ45098	Abq45098 Oligonucl
8	316.8	17.4	996	6 ABQ45099	Abq45099 Oligonucl
9	301	16.6	996	6 ABQ45100	Abq45100 Oligonucl
10	301	16.6	996	6 ABQ45101	Abq45101 Oligonucl
11	171	9.4	4901	4 ABL05477	Ab105477 Drosophil
12	171	9.4	4901	10 ADK11343	Adk11343 Drosophil
13	99.2	5.5	8256	4 ABL05476	Ab105476 Drosophil
14	62	3.4	62	13 ADR00046	Adr00046 PPM1D PCR
15	60	3.3	60	6 ABN58833	Abn58833 Human spl
16	60	3.3	60	6 ABN58576	Abn58576 Human spl
17	60	3.3	60	6 ABN38820	Abn38820 Human spl
18	60	3.3	60	6 ABN58577	Abn58577 Human spl
19	57.6	3.2	2000	8 ADA71938	Ada71938 Rice gene

20	52.6	2.9	2974	2	AAQ79630	AAQ79630 Partial F
21	51.2	2.8	15738	10	ADI23932	ADI23932 Streptomy
22	51.2	2.8	61944	10	ADI23920	ADI23920 Streptomy
23	50.8	2.8	32329	12	ADO51695	ADO51695 Streptomy
24	50.4	2.8	3240	14	AE91819	AE91819 DNA encod
25	50.4	2.8	110000	4	AAI99682_39	Continuation (40 o
26	50.4	2.8	110000	4	AAI99683_39	Continuation (40 o
27	48.2	2.7	13695	3	ABN97984	ABN97984 FMR2 codi
28	47.8	2.6	444	14	ADV90740	Adv90740 Cow milk
29	47.6	2.6	114955	2	AAX53491	Aax53491 Human ade
30	47.2	2.6	889	13	ADT19227	Adt19227 Plant cDN
31	47.2	2.6	2535	10	AAD51682	Aad51682 Human nuc
32	47.2	2.6	15624	13	ADQ91707	Adq91707 Polyketid
33	47.2	2.6	15624	13	AE86999	AE86999 Streptomy
34	47.2	2.6	15624	13	AE86796	AE86796 Streptomy
35	47.2	2.6	164051	13	ADQ91695	Adq91695 Polyketid
36	47.2	2.6	164051	13	AE86862	AE86862 Streptomy
37	47.2	2.6	164051	13	AE86659	AE86659 Streptomy
38	47	2.6	1287	12	ADJ39845	Adj39845 Plant cDN
39	47	2.6	2000	8	ADA71539	Ada71539 Rice gene
40	46.4	2.6	688	2	AAV34216	Aav34216 Human sec
41	46.4	2.6	688	8	ACD08087	Acd08087 cDNA enco
42	46.4	2.6	688	14	ADZ12273	Adz12273 Human sec
43	46.4	2.6	2000	11	ACL36471	ACL36471 Rice stre
44	46.2	2.5	24081	10	AAD54223	Aad54223 Streptomy
45	46.2	2.5	52101	10	AAD54217	Aad54217 Streptomy
46	46	2.5	987	12	ADI42117	Adi42117 Plant tra
47	46	2.5	987	12	ADO02664	Ado02664 Corn orth
48	45.8	2.5	321	5	AAD13973	Aad13973 Human 5'
49	45.8	2.5	700	3	AAA37651	Aaa37651 FMR1 gene
50	45.8	2.5	1755	13	ADT42104	Adt42104 Bacterial
51	45.6	2.5	2160	14	AE12322	Aeb12322 Human HCN
52	45.6	2.5	2670	14	AE12298	Aeb12298 Human HCN
53	45.6	2.5	3372	13	ADQ83419	Adq83419 Human tum
54	45.6	2.5	3431	4	AAH98302	Aah98302 Human EST
55	45.6	2.5	3459	6	AAD29756	Aad29756 Human hyp
56	45.4	2.5	468	8	ACA37744	ACA37744 Prokaryot
57	45.4	2.5	777	12	ACH87329	Ach87329 Human gen
58	45.4	2.5	5208	14	ADY72593	Ady72593 A. orient
59	45.4	2.5	7599	11	ADM29297	Adm29297 Human nov
60	45.4	2.5	7847	11	ADM29295	Adm29295 Human nov
61	45.4	2.5	73599	14	ADY72575	Ady72575 Polyene p
62	45.2	2.5	705	11	ACL29071	ACL29071 Rice abio
63	45.2	2.5	728	12	ACH90930	Ach90930 Human gen
64	45.2	2.5	3132	14	ADZ49365	Adz49365 Insulin s
65	45.2	2.5	3632	2	AAV61586	Aav61586 Alpha-1A
66	45	2.5	2874	8	ACA40307	ACA40307 Prokaryot
67	45	2.5	6706	11	ADN95160	Adn95160 Human BEC
68	45	2.5	6706	12	ADQ20401	Adq20401 Human sof
69	45	2.5	6729	12	ADQ24402	Adq24402 Human sof
70	45	2.5	110000	4	AAI99682_03	Continuation (4 of
71	44.8	2.5	227968	6	ABK83497	Abk83497 Human cDN
72	44.8	2.5	227968	12	ADQ18538	Adq18538 Human sof
73	44.4	2.4	2160	14	AE12322	Aeb12322 Human HCN
74	44.4	2.4	2670	14	AE12298	Aeb12298 Human HCN
75	44.4	2.4	3372	13	ADQ83419	Adq83419 Human tum
76	44.4	2.4	3431	4	AAH98302	Aah98302 Human EST
77	44.4	2.4	3459	6	AAD29756	Aad29756 Human hyp
78	44.4	2.4	10144	6	ABN95670	Abn95670 Gene #216
79	44.2	2.4	1060	13	ADX31432	Adx31432 Plant ful
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81	44.2	2.4	114955	2	AAX53491	Aax53491 Human ade
82	44	2.4	966	14	AEA26884	Aea26884 Stress to
83	44	2.4	1427	8	ACD07381	Acd07381 Rice Myb-
84	44	2.4	1427	12	ADJ77726	Adj77726 cDNA enco
85	44	2.4	1813	2	AAV70895	Aav70895 cDNA enco
86	44	2.4	2079	4	AAD04199	Aad04199 Murine ha
87	44	2.4	2562	14	AE91823	Aeb91823 DNA encod
88	44	2.4	3453	14	ACL68250	ACL68250 M. xanthu
89	44	2.4	28762	14	ACL64769	ACL64769 M. xanthu
90	44	2.4	110000	4	AAI99682_12	Continuation (13 o
91	43.8	2.4	357	8	ABX49504	Abx49504 Bovine ES
92	43.8	2.4	1623	14	ACL65588	ACL65588 M. xanthu

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 13:46:36 ; Search time 9121.5 Seconds
(without alignments)
11329.436 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					%		Query		Match		Length		DB		ID		Description	
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1	1818	100.0	1818	6	AX662143												AX662143 Sequence	
2	1818	100.0	2902	8	BC016480												BC016480 Homo sapi	
3	1818	100.0	2973	6	AX662145												AX662145 Sequence	
4	1818	100.0	2973	6	AX777280												AX777280 Sequence	
5	1818	100.0	2973	8	HSU78305												U78305 Homo sapien	
6	1816.4	99.9	2865	8	BC033893												BC033893 Homo sapi	
7	1816.4	99.9	3001	8	BC060877												BC060877 Homo sapi	
8	1816	99.9	1818	8	BT009780												BT009780 Homo sapi	
9	1816	99.9	1818	11	AY888848												AY888848 Synthetic	
10	1816	99.9	1818	11	AY888849												AY888849 Synthetic	
11	1739.2	95.7	2169	8	AB168475												AB168475 Macaca fa	
12	1697	93.3	3070	8	BC042418												BC042418 Homo sapi	
13	1380	75.9	1968	9	AF200464												AF200464 Mus muscu	
14	1378.4	75.8	2908	9	BC051966												BC051966 Mus muscu	
15	1367.2	75.2	2023	9	BC023492												BC023492 Mus muscu	
16	615.4	33.9	876	5	CR406758												CR406758 Gallus ga	
c 17	560	30.8	160854	8	AC110602												AC110602 Homo sapi	
18	560	30.8	174711	14	AC025515												AC025515 Homo sapi	

